

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2003, 14:23:22 ; Search time 38 Seconds
(without alignments)
2955.149 Million cell updates/sec

Title: US-09-001-737-8

Perfect score: 2663

Sequence: 1 MAKEIKFSADARAAWYRGVD.....TPAPAMPAGMDPMWGMGNG 545

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_podent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2383.5	89.5	540	2	09AME7	09AME7 streptococ
2	2380	89.4	540	2	08VTS8	08VTS8 streptococ
3	2347	88.1	540	16	097NV4	097NV4 streptococ
4	2333	87.6	481	2	0337J3	0337J3 streptococ
5	2330	87.5	540	2	02X4K5	02X4K5 streptococ
6	2199	82.5	541	2	03AEV6	03AEV6 enterococc
7	2185.5	82.1	541	2	03AEV7	03AEV7 lactococc
8	2015.5	75.8	539	2	08RCV0	08RCV0 bacillus sp
9	2011.5	75.5	539	2	08VVC4	08VVC4 bacillus th
10	2003.5	75.2	544	2	02E2V4	02E2V4 lactobacill
11	1999.5	75.1	544	2	032847	032847 lactobacill
12	1985	74.5	535	2	093GV6	093GV6 tetragenoco
13	1948	73.2	543	2	09KJ23	09KJ23 lactobacill
14	1905	71.5	538	16	099SL7	099SL7 staphylococ
15	1887	70.9	525	2	08VTW6	08VTW6 staphylococ
16	1877	70.5	525	2	08VTW8	08VTW8 staphylococ

17	1868.5	70.2	543	2	08RU00	08RU00 brevibacill
18	1850.5	69.5	546	2	093G07	093G07 lactobacill
19	1767.5	66.4	540	2	09KRF0	09KRF0 clostridium
20	1759.5	66.1	540	2	09KJV7	09KJV7 clostridium
21	1701.5	63.9	541	2	09KGM1	09KGM1 mycobacteri
22	1699	63.8	540	16	08RST7	08RST7 thermococ
23	1691.5	63.5	546	2	031198	031198 leptospira
24	1691.5	63.5	548	2	087888	087888 leuconia in
25	1690	63.5	551	16	098354	098354 rhizobium 1
26	1687	63.3	548	16	09RW09	09RW09 delonococc
27	1681.5	63.1	541	16	08R5X7	08R5X7 streptococ
28	1672.5	62.8	541	16	09KXU5	09KXU5 streptococ
29	1668.5	62.7	537	2	09K171	09K171 bifidobacte
30	1664.5	62.5	546	2	08RT77	08RT77 xanthomonas
31	1661.5	62.4	546	16	08RT53	08RT53 bruceella me
32	1660.5	62.4	546	2	093MH1	093MH1 rhodospseud
33	1659.5	62.3	532	16	098AX9	098AX9 rhodochermu
34	1657	62.2	540	2	09KCA9	09KCA9 rhizobium 1
35	1657	62.2	542	2	09L691	09L691 rhizobium 1
36	1657	62.2	549	16	0981J9	0981J9 bifidobacte
37	1655.5	62.1	538	2	09EX76	09EX76 propionibac
38	1654.5	62.1	533	2	09PDS2	09PDS2 pseudonater
39	1649.5	61.9	549	2	09AJB5	09AJB5 corynebacte
40	1648	61.9	541	2	093Q12	093Q12 rhizobium 1
41	1648	61.9	542	16	0981H9	0981H9 rhizobium 1
42	1647.5	61.9	548	2	09L7P5	09L7P5 vibrio para
43	1645.5	61.8	545	2	093RU8	093RU8 enterococ
44	1644.5	61.8	538	2	09EZV1	09EZV1 thermococ
45	1642.5	61.7	560	16	08VTS8	08VTS8 anabaena sp

ALIGNMENTS

RESULT 1

09AME7 PRELIMINARY: PRT: 540 AA.

AC 09AME7;
BT 01-JUN-2001 (TREMBLrel. 17, Created)
BT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
BT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RA Jwo-Farr C.;
RT "Cloning, sequencing, and characterization of 60 kDa Chaperonin gene from Streptococcus agalactiae".
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC EMBL: AF352222; AK12938.1; .
CC HSSP: P06139; IGRU.
CC InterPro: IPR001844; Chpn6n_Cpn60.
CC InterPro: IPR002423; Cpn60_TCP-1.
CC Pfam: PF00118; Cpn60_TCP1.1.
CC PRINTS: PR00298; CHAPERONIN60.
CC PROSITE: PS00304; TCOMPLEXTCP1.
CC ATP-binding: Chaperone.
CC KW SEQUENCE 540 AA; 57287 MW; F3920855CF919ND1 CRC64;

Query Match 89.5%; Score 2383.5; DB 2; Length 540;
Best local similarity 89.7%; Pred. No. 2.4e-105;
Matches 486; Conservative 25; Mismatches 26; Indels 3; Gaps 2;

```

OY 1 MAKEIFSADARAAMVGVMDLADTVKTLGPKGRNVYLEKAFSGPLITNDGVTIAKEIE 60
DB 1 MANDIKFSADARSAMVGVMDLADTVKTLGPKGRNVYLEKAFSGPLITNDGVTIAKEIE 60
OY 61 LEHFEFNKAGLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNTAGANPIGIRGIE 120
DB 61 LEHFEFNKAGLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNTAGANPIGIRGIE 120
OY 121 TATATVEALKAIQAPVSGKEALAOVAASRSREKVEYISEAMERVNGDVTITEESRG 180
DB 121 TATATVEALKAIQAPVSGKEALAOVAASRSREKVEYISEAMERVNGDVTITEESRG 180
OY 181 METELEVEGMOFDRGLTSQYMTDNKEMVADLENPILITDKVSNIDILPLEEVLK 240
DB 181 METELEVEGMOFDRGLTSQYMTDNKEMVADLENPILITDKVSNIDILPLEEVLK 240
OY 241 TNRPLLIADVDGEALPTLVNKRIGTFNVAVAKPGFDRRAMLEDAITLGTGVTIT 300
DB 241 TNRPLLIADVDGEALPTLVNKRIGTFNVAVAKPGFDRRAMLEDAITLGTGVTIT 300
OY 301 EDLGLDKATMTALGOAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPDR 360
DB 301 EDLGLDKATMTALGOAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPDR 360
OY 361 EKLQERLAKLVAGVAVIKVGAFTETALKEMKLRIEDALNATRAAVEGIVAGGTAITV 420
DB 361 EKLQERLAKLVAGVAVIKVGAFTETALKEMKLRIEDALNATRAAVEGIVAGGTAITV 420
OY 421 IEKVALELEGGDAGTGRNIVYALALEEPYROIALNAGYEGSVYIDKLKNSPAGTGNATG 480
DB 421 IEKVALELEGGDAGTGRNIVYALALEEPYROIALNAGYEGSVYIDKLKNSPAGTGNATG 480
OY 481 EMDMKTGIIIDPKYKTRSAONASVASLITTEAVVANKPEPATPAPAMPADPMGM 540
DB 481 EMDMKTGIIIDPKYKTRSAONASVASLITTEAVVANKPEPATPAPAMPADPMGM 540
OY 541 GGM 543
DB 541 GGM 543
OY 537 GGM 539
DB 537 GGM 539

```

RESULT 2

```

OQ9758 PRELIMINARY; PRT; 540 AA.
AC 08VTS8;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE GROEL.
OS Streptococcus gordonii.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1302;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC10558;
RA Teng L.-J. Hsu J.-C.;
RT "The groESL of Streptococcus gordonii ATCC 10558."
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF38228; MAL73234.1;
DR InterPro: IPR001844; Chaperlin_Cpn60.
DR Pfam: PF00118; Cpn60_TCP1.1;
DR PRINTS: PR00298; CHAPERONIN60.
DR POSSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
SQ SOURCE 540 AA: 56769 MW: EAA47712767CFC39 CRC64;
Query Match 89.4%, Score 2380; DB 2; Length 540;
Best Local Similarity 88.2%, Pred. No. 3,6e-105;
Matches 479; Conservative 39; Mismatches 21; Indels 4; Gaps 1;
OY 1 MAKEIFSADARAAMVGVMDLADTVKTLGPKGRNVYLEKAFSGPLITNDGVTIAKEIE 60

```

```

DB 1 MANDIKFSADARSAMVGVMDLADTVKTLGPKGRNVYLEKAFSGPLITNDGVTIAKEIE 60
OY 61 LEHFEFNKAGLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNTAGANPIGIRGIE 120
DB 61 LEHFEFNKAGLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNTAGANPIGIRGIE 120
OY 121 TATATVEALKAIQAPVSGKEALAOVAASRSREKVEYISEAMERVNGDVTITEESRG 180
DB 121 TATATVEALKAIQAPVSGKEALAOVAASRSREKVEYISEAMERVNGDVTITEESRG 180
OY 181 METELEVEGMOFDRGLTSQYMTDNKEMVADLENPILITDKVSNIDILPLEEVLK 240
DB 181 METELEVEGMOFDRGLTSQYMTDNKEMVADLENPILITDKVSNIDILPLEEVLK 240
OY 241 TNRPLLIADVDGEALPTLVNKRIGTFNVAVAKPGFDRRAMLEDAITLGTGVTIT 300
DB 241 TNRPLLIADVDGEALPTLVNKRIGTFNVAVAKPGFDRRAMLEDAITLGTGVTIT 300
OY 301 EDLGLDKATMTALGOAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPDR 360
DB 301 EDLGLDKATMTALGOAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPDR 360
OY 361 EKLQERLAKLVAGVAVIKVGAFTETALKEMKLRIEDALNATRAAVEGIVAGGTAITV 420
DB 361 EKLQERLAKLVAGVAVIKVGAFTETALKEMKLRIEDALNATRAAVEGIVAGGTAITV 420
OY 421 IEKVALELEGGDAGTGRNIVYALALEEPYROIALNAGYEGSVYIDKLKNSPAGTGNATG 480
DB 421 IEKVALELEGGDAGTGRNIVYALALEEPYROIALNAGYEGSVYIDKLKNSPAGTGNATG 480
OY 481 EMDMKTGIIIDPKYKTRSAONASVASLITTEAVVANKPEPATPAPAMPADPMGM 540
DB 481 EMDMKTGIIIDPKYKTRSAONASVASLITTEAVVANKPEPATPAPAMPADPMGM 540
OY 541 GGM 543
DB 541 GGM 543
OY 537 GGM 539
DB 537 GGM 539

```

RESULT 3

```

OQ97N4 PRELIMINARY; PRT; 540 AA.
AC 097N4;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Chaperonin, 60 kDa (GroEL).
OS Streptococcus pneumoniae.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIGR4;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Duxkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Duxman L.A., White O., Salzberg S.L., Lewis M.R., Redune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Ullrich T.R., Hansen C.B.,
RA McDonald L.A., Feldblyum T.V., Angluoi S., Dickinson T., Hackey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-ESP174;
RA Dupond D.F., Young A., Wright J.A.;
RT "Molecular chaperones/chaperonin-encoding stress genes groEL and groES

```

Wed Apr 16 08:08:22 2003

us-09-001-737-8.rpt

Page 3

RT and their use as antimicrobial targets.
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF007482; AAK75976.1;
DR EMBL: AF325449; AAL55997.1;
DR TIGR: SPI906;
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXCP1.
DR PROSITE: PS00296; CHAPERONIN_CPN60; 1.
DR Complete proteome.
KM SEQUENCE 340 AA; 57095 MW; EBA6CB19C0CD894C CRC64;
SO
Query Match 88.1%; Score 2347; DB 16; Length 540;
Best Local Similarity 87.8%; Pred. No. 1,3e-103;
Matches 477; Conservative 34; Mismatches 28; Indels 4; Gaps 1;
QY 1 MAKEIKFSADARAAMVGVDMADTVKTLGPKGRNVYLEKAFGSLITNGVTIAKEIE 60
DB 1 MSKEIKFSADARAAMVGVDMADTVKTLGPKGRNVYLEKAFGSLITNGVTIAKEIE 60
QY 61 LEDHFNMGAKLYSEVASKTNDIAGDGTATATVLTQAIYHEGLKNTAGANPGRIGIE 120
DB 61 LEDHFNMGAKLYSEVASKTNDIAGDGTATATVLTQAIYHEGLKNTAGANPGRIGIE 120
QY 121 TATAVEALKKAIAOPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
DB 121 TATAVEALKKAIAOPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
QY 122 TATAVEALKKAIAOPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
DB 122 TATAVEALKKAIAOPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
QY 181 METELEVEGMOFDRGYLSQMTVDNEKNVADLENPELITLTKKVSNTIDILPLEEVLK 240
DB 181 METELEVEGMOFDRGYLSQMTVDNEKNVADLENPELITLTKKVSNTIDILPLEEVLK 240
QY 241 TNRPLLIADVDGALPTVLNKRIGTFNVAAVAKAGFDRRKAMEIDAIITGTVIT 300
DB 241 SNRPLLIADVDGALPTVLNKRIGTFNVAAVAKAGFDRRKAMEIDAIITGTVIT 300
QY 301 EDGLKELKDATMTALGQAARTVDKSTVIEGSGSSEAIANRIALIKSOLETTSSDDR 360
DB 301 EDGLKELKDATMTALGQAARTVDKSTVIEGSGSSEAIANRIALIKSOLETTSSDDR 360
QY 361 EKLDERLAKIAGGVAIVKGAFTETALKEMKLRIEDALNTRAAGEIVAGGTAITLV 420
DB 361 EKLDERLAKIAGGVAIVKGAFTETALKEMKLRIEDALNTRAAGEIVAGGTAITLV 420
QY 421 IEKVALEEGDDATGRIVLRALPEPVOIALNAGEGSVYIDKLNSPAGTGFMATG 480
DB 421 IPAVATLELGDATGRIVLRALPEPVOIALNAGEGSVYIDKLNSPAGTGFMATG 480
QY 481 EYDMITGIIIDPVKTRSRALONASVASLITTEAVANKKEPATAPAMPAGMDPGMM 540
DB 481 EYDMITGIIIDPVKTRSRALONASVASLITTEAVANKKEPATAPAMPAGMDPGMM 540
QY 541 GGM 543
DB 537 GGM 539
RESULT 4
ID 033733 PRELIMINARY; PRT: 481 AA.
AC 033733;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein) (Fragment).
GN GROEL.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1314;
RN [1]

RP SEQUENCE FROM N.A.
RA Pohl B., Podbelski A., Zarges I.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: X89236; CAA61520.1;
DR HSP; P06139; 1GR1.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXCP1.
DR PROSITE: PS00296; CHAPERONIN_CPN60; 1.
KM ATP-binding; Chaperone.
FT NON_TER
SO SEQUENCE 481 AA; 50496 MW; FA80BB97CA7B6D11 CRC64;
Query Match 87.6%; Score 2333; DB 2; Length 481;
Best Local Similarity 99.4%; Pred. No. 5.1e-103;
Matches 477; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 63 DHEFNMGAKLYSEVASKTNDIAGDGTATATVLTQAIYHEGLKNTAGANPGRIGIE 122
DB 1 DHEFNMGAKLYSEVASKTNDIAGDGTATATVLTQAIYHEGLKNTAGANPGRIGIE 122
QY 123 TATAVEALKKAIAOPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 182
DB 61 TATAVEALKKAIAOPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 120
QY 183 TELEVEGMOFDRGYLSQMTVDNEKNVADLENPELITLTKKVSNTIDILPLEEVLK 242
DB 121 TELEVEGMOFDRGYLSQMTVDNEKNVADLENPELITLTKKVSNTIDILPLEEVLK 180
QY 243 RPLLIADVDGALPTVLNKRIGTFNVAAVAKAGFDRRKAMEIDAIITGTVIT 302
DB 181 RPLLIADVDGALPTVLNKRIGTFNVAAVAKAGFDRRKAMEIDAIITGTVIT 240
QY 303 LGLELKDATMTALGQAARTVDKSTVIEGSGSSEAIANRIALIKSOLETTSSDDR 362
DB 241 LGLELKDATMTALGQAARTVDKSTVIEGSGSSEAIANRIALIKSOLETTSSDDR 300
QY 363 LOERLAKIAGGVAIVKGAFTETALKEMKLRIEDALNTRAAGEIVAGGTAITLV 422
DB 301 LOERLAKIAGGVAIVKGAFTETALKEMKLRIEDALNTRAAGEIVAGGTAITLV 360
QY 423 KVALELEGGDDATGRIVLRALPEPVOIALNAGEGSVYIDKLNSPAGTGFMATG 482
DB 361 KVALELEGGDDATGRIVLRALPEPVOIALNAGEGSVYIDKLNSPAGTGFMATG 420
QY 483 VDMITGIIIDPVKTRSRALONASVASLITTEAVANKKEPATAPAMPAGMDPGMM 542
DB 421 VDMITGIIIDPVKTRSRALONASVASLITTEAVANKKEPATAPAMPAGMDPGMM 480
RESULT 5
ID 09X4R5 PRELIMINARY; PRT: 540 AA.
AC 09X4R5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
GN GROEL.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactob
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1313;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CP1200;
 RA Kim S.N., Lee J.Y., Kim S.W., Choi I.H., Rhee D.K.;
 RT "groEL" sequences in *Streptococcus pneumoniae*;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR EMBL: AF117741; AAD3455.1; -
 DR HSP60; P06139; IGRU.
 DR InterPro: IPR001844; Chaprin.Cpn60.
 DR InterPro: IPR002423; Cpn60.TCP.1.
 DR Pfam: PF00118; Cpn60.TCP.1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCNPLETICP1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60.1.
 DR ATP-binding; Chaperone.
 KM SEQUENCE 540 AA: 57213 MW: 4CDB489AF1C632DA CRC64;
 Query Match 87.5%; Score 2330; DB 2; Length 540;
 Best Local Similarity 87.1%; Pred. No. 8,3e-103;
 Matches 473; Conservative 36; Mismatches 30; Indels 4; Gaps 1;
 QY 1 MAKEIKESADARAARAVRGVMDLADTVKVTLPGRKNVYLEKAFSGPLITNDGVTAKKE 60
 DB 1 MSKEIKSSDARSAMRGVDILADTVKVTLPGRKNVYLEKAFSGPLITNDGVTAKKE 60
 QY 61 LEDHEFMGKLYSEVASKTNDIAGDGTATVTLQAIYHEGINKNTAGANPIGIRGIE 120
 DB 61 LEDHEFMGKLYSEVASKTNDIAGDGTATVTLQAIYHEGINKNTAGANPIGIRGIE 120
 QY 121 TATATVAELKAIAPVSGKEAIAQVAAYSSRSKVEYISPMERVNGDGVITIEESRG 180
 DB 121 TATATVAELKAIAPVSGKEAIAQVAAYSSRSKVEYISPMERVNGDGVITIEESRG 180
 QY 122 TATAVAELKAIAPVSGKEAIAQVAAYSSRSKVEYISPMERVNGDGVITIEESRG 180
 DB 122 TATAVAELKAIAPVSGKEAIAQVAAYSSRSKVEYISPMERVNGDGVITIEESRG 180
 QY 181 METELEVEGMPFDGYSQYMTDNEKNVADLENPFILITDKKYSNIDILPLEEVLK 240
 DB 181 METELEVEGMPFDGYSQYMTDNEKNVADLENPFILITDKKYSNIDILPLEEVLK 240
 QY 181 METELEVEGMPFDGYSQYMTDNEKNVADLENPFILITDKKYSNIDILPLEEVLK 240
 DB 181 METELEVEGMPFDGYSQYMTDNEKNVADLENPFILITDKKYSNIDILPLEEVLK 240
 QY 241 TNRPLLIADVDGALPTLVNKRIGTFNVVAKAPGGRKRMLEDIAILITGTYIT 300
 DB 241 SNRPLLIADVDGALPTLVNKRIGTFNVVAKAPGGRKRMLEDIAILITGTYIT 300
 QY 301 EDLGELEKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 DB 301 EDLGELEKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 QY 361 EKLDERLAKIAGVAVIKVGAFTETALKEMKRIEDALNATRAVEGIVAGGCTALITV 420
 DB 361 EKLDERLAKIAGVAVIKVGAFTETALKEMKRIEDALNATRAVEGIVAGGCTALITV 420
 QY 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVIDKLKNSPAGTGFNAATG 480
 DB 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVIDKLKNSPAGTGFNAATG 480
 QY 481 EWMVMKITGIIPVYTRSAALONAASVASLITTEAVVANKPEPATPAMPAGNDGGM 540
 DB 481 EWMVMKITGIIPVYTRSAALONAASVASLITTEAVVANKPEPATPAMPAGNDGGM 540
 QY 541 GGM 543
 DB 537 GGM 539

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE GROEL.
 GN Enterococcus faecalis (*Streptococcus faecalis*).
 OS Bacteria: Firmicutes: Bacillus/Clostridium group; Lactobacillales;
 OC Enterococaceae: Enterococcus.
 CX NCBI_TaxID=1351;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29212;
 RX MEDLINE=2147444; PubMed=11526171.
 RA Tang J.J., Hsueh P.R., Wang F.H., Lin H.M., Luh K.T., Ho S.W.;
 RT Determination of Enterococcus faecalis groEL full-length sequence
 RT and Application for Species Identification.
 RL J. Clin. Microbiol. 39:3326-3331(2001).
 DR EMBL: AF35185; AAL04033.1; -
 DR InterPro: IPR001844; Chaprin.Cpn60.
 DR InterPro: IPR002423; Cpn60.TCP.1.
 DR Pfam: PF00118; Cpn60.TCP.1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR ATP-binding; Chaperone.
 KM SEQUENCE 541 AA: 57052 MW: 6086A0C92075AB17 CRC64;
 Query Match 82.4%; Score 2194; DB 2; Length 541;
 Best Local Similarity 81.7%; Pred. No. 2,3e-96;
 Matches 445; Conservative 46; Mismatches 48; Indels 6; Gaps 2;
 QY 1 MAKEIKESADARAARAVRGVMDLADTVKVTLPGRKNVYLEKAFSGPLITNDGVTAKKE 60
 DB 1 MAKEIKESADARAARAVRGVMDLADTVKVTLPGRKNVYLEKAFSGPLITNDGVTAKKE 60
 QY 61 LEDHEFMGKLYSEVASKTNDIAGDGTATVTLQAIYHEGINKNTAGANPIGIRGIE 120
 DB 61 LEDHEFMGKLYSEVASKTNDIAGDGTATVTLQAIYHEGINKNTAGANPIGIRGIE 120
 QY 121 TATATVAELKAIAPVSGKEAIAQVAAYSSRSKVEYISPMERVNGDGVITIEESRG 180
 DB 121 TATATVAELKAIAPVSGKEAIAQVAAYSSRSKVEYISPMERVNGDGVITIEESRG 180
 QY 122 TATAVAELKAIAPVSGKEAIAQVAAYSSRSKVEYISPMERVNGDGVITIEESRG 180
 DB 122 TATAVAELKAIAPVSGKEAIAQVAAYSSRSKVEYISPMERVNGDGVITIEESRG 180
 QY 181 METELEVEGMPFDGYSQYMTDNEKNVADLENPFILITDKKYSNIDILPLEEVLK 240
 DB 181 IETELDVEGMPFDGYSQYMTDNEKNVADLENPFILITDKKYSNIDILPLEEVLK 240
 QY 241 TNRPLLIADVDGALPTLVNKRIGTFNVVAKAPGGRKRMLEDIAILITGTYIT 300
 DB 241 QSRPLLIADVDGALPTLVNKRIGTFNVVAKAPGGRKRMLEDIAILITGTYIT 300
 QY 301 EDLGELEKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 DB 301 EDLGELEKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 QY 361 EKLDERLAKIAGVAVIKVGAFTETALKEMKRIEDALNATRAVEGIVAGGCTALITV 420
 DB 361 EKLDERLAKIAGVAVIKVGAFTETALKEMKRIEDALNATRAVEGIVAGGCTALITV 420
 QY 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVIDKLKNSPAGTGFNAATG 480
 DB 421 IGKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVIDKLKNSPAGTGFNAATG 480
 QY 481 EWMVMKITGIIPVYTRSAALONAASVASLITTEAVVANKPEPATPAMPAGNDGGM 540
 DB 481 EWMVMKITGIIPVYTRSAALONAASVASLITTEAVVANKPEPATPAMPAGNDGGM 540
 QY 541 GGM 545
 DB 536 -GNG 539

RESULT 6
 Q93E06 PRELIMINARY: PRT: 541 AA.
 AC Q93E06
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

RESULT 7
 Q9AEP7 PRELIMINARY: PRT: 542 AA.
 AC Q9AEP7
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

01-JUN-2001 (Tremblrel. 17, last annotation update)
01-MAR-2002 (Tremblrel. 20, last annotation update)
60 kDa chaperonin (protein Cpn60) (GroEL protein).
Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales.
Streptococcaceae; Lactococcus.
NCBI_Taxid=1359;
RN
SEQUENCE FROM N.A.
RC STRAIN-MG1363;
RA Vogensen F.K.; Kilstrup M.;
RT "GroELs sequence from Lactococcus lactis subsp. cremoris MG1363.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AY029215; AKK1639.1;
DR HSP: P06139; IGR1.
DR Interpro: IPR001844; Chaperin_Cpn60.
DR Interpro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR Pfam: PF00298; CHAPERONIN60.
DR PRINTS: PRO0304; TCOMPLEXCPI.
DR PROSITE: PS00296; CHAPERONIN5_CPN60.1.
DR ATP-binding; Chaperone.
KW SEQUENCE 542 AA; 57196 MW; EA81C4432EAFCA1 CRC64;
Query Match 82.1%; Score 2185.5; DB 2; Length 542;
Best Local Similarity 81.1%; Pred. No. 5,8e-96;
Matches 442; Conservative 49; Mismatches 49; Indels 5; Gaps 3;
1 MAKEIKFSADARAAMRGVMDLADYKVTGPGKRVNVEKRFSPPLITNDGYTIKKE 60
1 MSKEIKFSADARTAMRGIDILADYKVTGPGKRVNVEKSGSPPLITNDGYTIKKE 60
61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATVTAQIYHEGKLVNAGANPIGIRGIE 120
61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATVTAQIYHEGKLVNAGANPIGIRGIE 120
61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATVTAQIYHEGKLVNAGANPIGIRGIE 120
121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYSISAMERGVNDGYTIEESRG 160
121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYSISAMERGVNDGYTIEESRG 160
121 LAETVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYSISAMERGVNDGYTIEESRG 160
181 METELEVEVEGQDFRGYLSQYVNTDNEKVAADLENPILITDKKVSNIODILPLEEVLK 240
181 METELEVEVEGQDFRGYLSQYVNTDNEKVAADLENPILITDKKVSNIODILPLEEVLK 240
181 METELEVEVEGQDFRGYLSQYVNTDNEKVAADLENPILITDKKVSNIODILPLEEVLK 240
241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGRRKAMLEDAITLTGTYIT 300
241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGRRKAMLEDAITLTGTYIT 300
241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGRRKAMLEDAITLTGTYIT 300
301 EDLGLELKDAMTALGOAAKITVDKSTVIYEGSGSEALNARIALIKSOLETTSDPR 360
301 EDLGLELKDAMTALGOAAKITVDKSTVIYEGSGSEALNARIALIKSOLETTSDPR 360
301 EDLGLELKDAMTALGOAAKITVDKSTVIYEGSGSEALNARIALIKSOLETTSDPR 360
361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGSIYAGGGATLTV 420
361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGSIYAGGGATLTV 420
361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGSIYAGGGATLTV 420
421 IEKVAALTEEGDDATGRNIVLRALIEEPVROIALNAGTEGSSVYIDKLSNAGCGNATG 480
421 IEKVAALTEEGDDATGRNIVLRALIEEPVROIALNAGTEGSSVYIDKLSNAGCGNATG 480
421 IEKVAALTEEGDDATGRNIVLRALIEEPVROIALNAGTEGSSVYIDKLSNAGCGNATG 480
481 EMDMIRKIGLIDPVKVTIRSLQNAASVSLITTEAVANKEPATAPAMPAGDPCGM 540
481 EMDMIRKIGLIDPVKVTIRSLQNAASVSLITTEAVANKEPATAPAMPAGDPCGM 540
481 EMDMIRKIGLIDPVKVTIRSLQNAASVSLITTEAVANKEPATAPAMPAGDPCGM 540
541 GGMG 545
537 -GMG 540

RESULT 8
ID Q9RC20 PRELIMINARY; PRT; 539 AA.
AC Q9RC20;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE 60 kDa chaperonin (protein Cpn60) (GroEL protein).
GN Cpn60.
OS Bacillus sp. MS.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_Taxid=96470;
RN
SEQUENCE FROM N.A.
RC STRAIN-MS.
RA Kondo A.; Yoshida M.;
RT Cpn60/10 from Bacillus strain MS.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AB028452; BAA88110.1;
DR HSP: P06139; IGR1.
DR Interpro: IPR001844; Chaperin_Cpn60.
DR Interpro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PRO0298; CHAPERONIN60.
DR PRINTS: PRO0304; TCOMPLEXCPI.
DR PROSITE: PS00296; CHAPERONIN5_CPN60.1.
DR ATP-binding; Chaperone.
KW SEQUENCE 539 AA; 57346 MW; 95626C980E30C46F CRC64;
Query Match 75.8%; Score 2019.5; DB 2; Length 539;
Best Local Similarity 74.7%; Pred. No. 4.2e-88;
Matches 407; Conservative 63; Mismatches 66; Indels 9; Gaps 2;
1 MAKEIKFSADARAAMRGVMDLADYKVTGPGKRVNVEKRFSPPLITNDGYTIKKE 60
1 MAKEIKFSADARAAMRGVMDLADYKVTGPGKRVNVEKRFSPPLITNDGYTIKKE 60
61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATVTAQIYHEGKLVNAGANPIGIRGIE 120
61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATVTAQIYHEGKLVNAGANPIGIRGIE 120
61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATVTAQIYHEGKLVNAGANPIGIRGIE 120
121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYSISAMERGVNDGYTIEESRG 180
121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYSISAMERGVNDGYTIEESRG 180
121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYSISAMERGVNDGYTIEESRG 180
181 METELEVEVEGQDFRGYLSQYVNTDNEKVAADLENPILITDKKVSNIODILPLEEVLK 240
181 METELEVEVEGQDFRGYLSQYVNTDNEKVAADLENPILITDKKVSNIODILPLEEVLK 240
181 METELEVEVEGQDFRGYLSQYVNTDNEKVAADLENPILITDKKVSNIODILPLEEVLK 240
241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGRRKAMLEDAITLTGTYIT 300
241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGRRKAMLEDAITLTGTYIT 300
241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGRRKAMLEDAITLTGTYIT 300
301 EDLGLELKDAMTALGOAAKITVDKSTVIYEGSGSEALNARIALIKSOLETTSDPR 360
301 EDLGLELKDAMTALGOAAKITVDKSTVIYEGSGSEALNARIALIKSOLETTSDPR 360
301 EDLGLELKDAMTALGOAAKITVDKSTVIYEGSGSEALNARIALIKSOLETTSDPR 360
361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGSIYAGGGATLTV 420
361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGSIYAGGGATLTV 420
361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGSIYAGGGATLTV 420
421 IEKVAALTEEGDDATGRNIVLRALIEEPVROIALNAGTEGSSVYIDKLSNAGCGNATG 480
421 IEKVAALTEEGDDATGRNIVLRALIEEPVROIALNAGTEGSSVYIDKLSNAGCGNATG 480
421 IEKVAALTEEGDDATGRNIVLRALIEEPVROIALNAGTEGSSVYIDKLSNAGCGNATG 480
481 EMDMIRKIGLIDPVKVTIRSLQNAASVSLITTEAVANKEPATAPAMPAGDPCGM 540
481 EMDMIRKIGLIDPVKVTIRSLQNAASVSLITTEAVANKEPATAPAMPAGDPCGM 540
481 EMDMIRKIGLIDPVKVTIRSLQNAASVSLITTEAVANKEPATAPAMPAGDPCGM 540
541 GGMG 545
537 -GMG 540

```

QY 481 EMDVMTGIIIDPVKTRTSALQNAASVSLITTEAVANKREPAPAMPAGMDGK- 539
DB 481 EMDVMTGIIIDPVKTRTSALQNAASVSLITTEAVANKREPAPAMPAGMDGK- 539
QY 540 -MGCM 543
DB 534 DMGM 538

RESULT 9
QY 481 EMDVMTGIIIDPVKTRTSALQNAASVSLITTEAVANKREPAPAMPAGMDGK- 539
DB 481 EMDVMTGIIIDPVKTRTSALQNAASVSLITTEAVANKREPAPAMPAGMDGK- 539
QY 540 -MGCM 543
DB 534 DMGM 538

Query Match
Best Local Similarity 74.7%; Score 2011.5; DB 2: Length 539;
Matches 407; Conservative 62; Mismatches 67; Indels 9; Gaps 2;

QY 1 MAKEIFSADARAAMVGVMDLADTVKTLGPKGRNVLEKAFSGPLTNDGVTIAKEIE 60
DB 1 MAKEIFSADARAAMVGVMDLADTVKTLGPKGRNVLEKAFSGPLTNDGVTIAKEIE 60
QY 61 LEDHFNNGAKLYEVASKTNDIAGDGTATATVLTQAIYHSGLKNYTAGANPGRIGIE 120
DB 61 LEDHFNNGAKLYEVASKTNDIAGDGTATATVLTQAIYHSGLKNYTAGANPGRIGIE 120
QY 121 TATATVEALKAIAOPVSGKEALNOVAASVSEKGEYISEAMERGVNDGVITIEESRG 180
DB 121 TATATVEALKAIAOPVSGKEALNOVAASVSEKGEYISEAMERGVNDGVITIEESRG 180
QY 181 METELEVEGMOFQFQVLSQYWTNDKRNVADEENPFLITDKKVSNIQDILPLEEYVK 240
DB 181 METELEVEGMOFQFQVLSQYWTNDKRNVADEENPFLITDKKVSNIQDILPLEEYVK 240
QY 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGDRRKAMLEDAIILTGCVIT 300
DB 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGDRRKAMLEDAIILTGCVIT 300
QY 301 EDLGELEKDATATATLGOAAKITVDKSTIYVSGSSSEALANILILISOLETTSDPFR 360
DB 301 EDLGELEKDATATATLGOAAKITVDKSTIYVSGSSSEALANILILISOLETTSDPFR 360
QY 361 EELGRELKSTTIIASIGRASVYVTKENTIVGAGDSERIKANINOIAQLEETSEFGR 360
DB 361 EELGRELKSTTIIASIGRASVYVTKENTIVGAGDSERIKANINOIAQLEETSEFGR 360
QY 361 GLOGBRLAKLAGGVAVIVKAPFETALKEKRIEDLANTRAVEEGTVAGGTALMNV 420
DB 361 GLOGBRLAKLAGGVAVIVKAPFETALKEKRIEDLANTRAVEEGTVAGGTALMNV 420

```

```

QY 421 IEKVALEEGDADGRNIVLRALPEVROIALNAGYEGSVIDKLKNSPAGFPAATG 480
DB 421 YNKVALEAEAGDEATGVIVLRAIEPVRQIAQNAGLESGVYVERLSEKRGIGFAATG 480
QY 481 EMDVMTGIIIDPVKTRTSALQNAASVSLITTEAVANKREPAPAMPAGMDGK- 539
DB 481 EMDVMTGIIIDPVKTRTSALQNAASVSLITTEAVANKREPAPAMPAGMDGK- 539
QY 540 -MGCM 543
DB 534 DMGM 538

RESULT 10
QY 421 IEKVALEEGDADGRNIVLRALPEVROIALNAGYEGSVIDKLKNSPAGFPAATG 480
DB 421 YNKVALEAEAGDEATGVIVLRAIEPVRQIAQNAGLESGVYVERLSEKRGIGFAATG 480
QY 481 EMDVMTGIIIDPVKTRTSALQNAASVSLITTEAVANKREPAPAMPAGMDGK- 539
DB 481 EMDVMTGIIIDPVKTRTSALQNAASVSLITTEAVANKREPAPAMPAGMDGK- 539
QY 540 -MGCM 543
DB 534 DMGM 538

Query Match
Best Local Similarity 74.3%; Score 2003.5; DB 2: Length 539;
Matches 405; Conservative 63; Mismatches 68; Indels 9; Gaps 2;

QY 1 MAKEIFSADARAAMVGVMDLADTVKTLGPKGRNVLEKAFSGPLTNDGVTIAKEIE 60
DB 1 MAKEIFSADARAAMVGVMDLADTVKTLGPKGRNVLEKAFSGPLTNDGVTIAKEIE 60
QY 61 LEDHFNNGAKLYEVASKTNDIAGDGTATATVLTQAIYHSGLKNYTAGANPGRIGIE 120
DB 61 LEDHFNNGAKLYEVASKTNDIAGDGTATATVLTQAIYHSGLKNYTAGANPGRIGIE 120
QY 121 TATATVEALKAIAOPVSGKEALNOVAASVSEKGEYISEAMERGVNDGVITIEESRG 180
DB 121 TATATVEALKAIAOPVSGKEALNOVAASVSEKGEYISEAMERGVNDGVITIEESRG 180
QY 181 METELEVEGMOFQFQVLSQYWTNDKRNVADEENPFLITDKKVSNIQDILPLEEYVK 240
DB 181 METELEVEGMOFQFQVLSQYWTNDKRNVADEENPFLITDKKVSNIQDILPLEEYVK 240
QY 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGDRRKAMLEDAIILTGCVIT 300
DB 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGFGDRRKAMLEDAIILTGCVIT 300
QY 301 EDLGELEKDATATATLGOAAKITVDKSTIYVSGSSSEALANILILISOLETTSDPFR 360
DB 301 EDLGELEKDATATATLGOAAKITVDKSTIYVSGSSSEALANILILISOLETTSDPFR 360
QY 361 EELGRELKSTTIIASIGRASVYVTKENTIVGAGDSERIKANINOIAQLEETSEFGR 360
DB 361 EELGRELKSTTIIASIGRASVYVTKENTIVGAGDSERIKANINOIAQLEETSEFGR 360
QY 361 GLOGBRLAKLAGGVAVIVKAPFETALKEKRIEDLANTRAVEEGTVAGGTALMNV 420
DB 361 GLOGBRLAKLAGGVAVIVKAPFETALKEKRIEDLANTRAVEEGTVAGGTALMNV 420

```

OY 301 EDLGLKDATMTALGOAKITVDKDSIVYEGSSSEALANRILIKSOLETTSDPDR 360
 DB 301 FELGRLEKSTTASGRASAVYVTEKNTTIVEAGSDSKAKRIKQIADLESTSEDR 360
 OY 361 EKLQERLAKLAGVAVYKVGAPTEALKEMLKRIEDALNTRAAVEGIVAGGCTALTIV 420
 DB 361 EKLQERLAKLAGVAVYKVGAPTEALKEMLKRIEDALNTRAAVEGIVAGGCTALTIV 420
 OY 421 IEKVALELESGDAGTGRNIVYRALPEEPVQIALNAGIEGSSVIDKLKNSPAGTGMAATG 480
 DB 421 YSVAAIEEGDEATGVKIVYLAIEEPVQIALNAGIEGSSVIDKLKNSPAGTGMAATG 480
 OY 481 EYVDMIKTGIIDPVKVTRSALONNAAVSALITTEAVVANKPEPATPAPAMPAGMDPGM 539
 DB 481 EYVDMIKTGIIDPVKVTRSALONNAAVSALITTEAVVANKPEPATPAPAMPAGMDPGM 539
 OY 540 -MGCM 543
 DB 534 DMGCM 538

RESULT 11

ID 032847 PRELIMINARY: PRT: 544 AA.
 AC 032847;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
 GN GROEL.
 OS Lactobacillus zeae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Lactobacillaceae; Lactobacillus.
 OX NCBI_TaxID-57037;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1025;
 RA Murphy C.M., Chassy B.M.;
 RT "Molecular Characterization of the Heat-Shock Regulated groEL operon of Lactobacillus zeae."
 RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR EMBL: AF010281; AAB66326.1; -;
 DR HSP: P06139; IGR1.
 DR InterPro: IPR001844; Chaperin1n_Cpn60.
 DR InterPro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; Cpn60_TCF1.1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEXTCP1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60.1.
 KW ATP-binding; Chaperone.
 SQ SEQUENCE 544 AA; 57428 MW; AA2F544FAC2A1AF CRC64;

Query Match

Best Local Similarity 74.1%; Score 1999.5; DB 2; Length 544;
 Matches 404; Conservative 64; Mismatches 74; Indels 3; Gaps 2;

OY 1 MAKEITFSADARAARVGVDMADTVKVTGPGKGRNVYLEKAFSGPLITNDGVTIAKEIE 60
 DB 1 MAKEITFSADARAARVGVDMADTVKVTGPGKGRNVYLEKAFSGPLITNDGVTIAKEIE 60
 OY 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQIVHGLKANTVAGANPIGIRGIE 120
 DB 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQIVHGLKANTVAGANPIGIRGIE 120
 OY 121 TATATVAELAKIAOPVSGKEAIAQVAASRSSEKVGEXISEAERAGNDGVITTEESRG 180
 DB 121 TATATVAELAKIAOPVSGKEAIAQVAASRSSEKVGEXISEAERAGNDGVITTEESRG 180

DB 121 KATKANDELHKISRWKKEKIEIAQVAASSSNTFVSLADAMEKVGHDGVITTEESRG 180
 OY 181 METELEVEESMGDFRGYLSQYMTVDNEKNVADLENPILITDKVSNITODILPLEEVK 240
 DB 181 METELEVEESMGDFRGYLSQYMTVDNEKNVADLENPILITDKVSNITODILPLEEVK 240
 OY 241 TRPPLIADVDGEALPTLVNKRIGRTFNVAAPGDFDRKMLIEDIALILGCTVIT 300
 DB 241 OGRKALLIADVDGEALPTLVNKRIGRTFNVAAPGDFDRKMLIEDIALILGCTVIT 300
 OY 301 EDLGLKDATMTALGOAKITVDKDSIVYEGSSSEALANRILIKSOLETTSDPDR 360
 DB 301 EDLGLKDATMTALGOAKITVDKDSIVYEGSSSEALANRILIKSOLETTSDPDR 360
 OY 361 EKLQERLAKLAGVAVYKVGAPTEALKEMLKRIEDALNTRAAVEGIVAGGCTALTIV 420
 DB 361 EKLQERLAKLAGVAVYKVGAPTEALKEMLKRIEDALNTRAAVEGIVAGGCTALTIV 420
 OY 421 IEKVALELESGDAGTGRNIVYRALPEEPVQIALNAGIEGSSVIDKLKNSPAGTGMAATG 480
 DB 421 IEKVALELESGDAGTGRNIVYRALPEEPVQIALNAGIEGSSVIDKLKNSPAGTGMAATG 480
 OY 481 EYVDMIKTGIIDPVKVTRSALONNAAVSALITTEAVVANKPEPATPAPAMPAGMDPGM 540
 DB 481 EYVDMIKTGIIDPVKVTRSALONNAAVSALITTEAVVANKPEPATPAPAMPAGMDPGM 540
 OY 541 GCMG 545
 DB 538 AGMG 542

RESULT 12

ID 093GT6 PRELIMINARY: PRT: 535 AA.
 AC 093GT6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE GROEL.
 GN GROEL.
 OS Tetragenococcus halophilus (Pediococcus halophilus).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Enterococcaceae; Tetragenococcus.
 OX NCBI_TaxID-51669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fukuda D., Watanabe M., Aso Y., Sonomoto K., Ishizaki A.;
 RT "The groEL operon of halophilic lactic acid bacterium Tetragenococcus halophilus."
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB073399; BAB70661.1; -;
 DR InterPro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; Cpn60_TCF1.1.
 KW ATP-binding; Chaperone.
 SQ SEQUENCE 535 AA; 56893 MW; D9FF681CD3A4D17C CRC64;

Query Match

Best Local Similarity 74.5%; Score 1985; DB 2; Length 535;
 Matches 396; Conservative 73; Mismatches 58; Indels 12; Gaps 2;

OY 1 MAKEITFSADARAARVGVDMADTVKVTGPGKGRNVYLEKAFSGPLITNDGVTIAKEIE 60
 DB 1 MAKEITFSADARAARVGVDMADTVKVTGPGKGRNVYLEKAFSGPLITNDGVTIAKEIE 60
 OY 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQIVHGLKANTVAGANPIGIRGIE 120
 DB 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQIVHGLKANTVAGANPIGIRGIE 120
 OY 121 TATATVAELAKIAOPVSGKEAIAQVAASRSSEKVGEXISEAERAGNDGVITTEESRG 180
 DB 121 TATATVAELAKIAOPVSGKEAIAQVAASRSSEKVGEXISEAERAGNDGVITTEESRG 180
 OY 181 METELEVEESMGDFRGYLSQYMTVDNEKNVADLENPILITDKVSNITODILPLEEVK 240
 DB 181 METELEVEESMGDFRGYLSQYMTVDNEKNVADLENPILITDKVSNITODILPLEEVK 240

```

Db 177 IDLELVYVGNQDFRGYLSQYMTDNEKMEADDSFYLLITDKKISMDIPLLEQVYV 236
Qy 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVKAPGGRKRAKMEIDIALGGVIT 300
Db 237 ESKRPLIADIIDEALPTLVNKRIGTFNNVAVKAPGGRKRAKMEIDIALGGVIT 236
Qy 301 EDGELDKATMTALGQAKITVDKSTVIYEGSSSEAIANRIALIKSOLETTTSDPR 360
Db 297 EDGELDKATMTALGQAKITVDKSTVIYEGSSSEAIANRIALIKSOLETTTSDPR 356
Qy 361 EKLOERLAKLAGVAVIKVGAETELKEMKLRIEDALNATRAVEEGIVAGGCTALTIV 420
Db 357 EKLOERLAKLAGVAVIKVGAETELKEMKLRIEDALNATRAVEEGIVAGGCTALTIV 416
Qy 421 IEKVVALEEGDDA-TGRNIVYRALPEEPYQIALNAGYSGSVYIDKLKNSPAGTFNATG 480
Db 417 INNVALLADDAITGVNIVYRALPEEPYQIALNAGYSGSVYIDKLKNSPAGTFNATG 476
Qy 481 EMDVMTKGIIDPVKYVTSALONASVASLITTEVAANKPEPATPAMPACMDPGM 539
Db 477 QMNVNWDAGIVDPKYVTSALONASVASLITTEVAANKPEPATPAMPACMDPGM 527

RESULT 13
Qy 09KJ23 PRELIMINARY: PRT: 543 AA.
AC 09KJ23: 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein cpn60) (GroEL protein).
GN GROEL.
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Lactobacillaceae; Lactobacillus.
OX NCBI_TaxID=33959;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VPI 11088; PubMed=10388700;
RX MEDLINE=9318659; Pubmed=10388700;
RA Walker D.C., Girgis H.S., Kleenhammer T.R.;
RT "The groEL chaperone operon of Lactobacillus johnsonii.";
RL Appl. Environ. Microbiol. 65:3033-3041(1999).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC EMBL: AF214488; AAF75593.1;
DR HSP: P06139; IGR:
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP1.
DR Pfam: PF00118; Cpn60_TCP1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00104; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONIN_CPN60; UNKNOWN_1.
KW ATP-binding; Chaperone.
SQ
SD DEDUCE 543 AA: 57602 MW: BCEI69933CD0638 CRC64:

Query Match 73.2%; Score 1948; DB 2; Length 543;
Best Local Similarity 73.1%; Pred. No. 1e-84;
Matches 397; Conservative 62; Mismatches 76; Indels 8; Gaps 3;

```

```

Qy 121 TATAVEALKALAPVSGKEATAVOYAVSSRSKGEVYISFAMRNQDGVITIEESG 180
Db 122 TATAVADELHISIKVSTKDELTAQOYAVSSASSTEVGNLIRDMKQVHGVITIEESG 180
Qy 181 METLEEVNBPQFDGILSQYMTDNEKMEADDSFYLLITDKKISMDIPLLEQVYV 240
Db 181 IDLELVYVGNQDFRGYLSQYMTDNEKMEADDSFYLLITDKKISMDIPLLEQVYV 240
Qy 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVKAPGGRKRAKMEIDIALGGVIT 300
Db 241 QGKSLIADVDGEALPTLVNKRIGTFNNVAVKAPGGRKRAKMEIDIALGGVIT 300
Qy 301 EDLELEKATMTALGQAKITVDKSTVIYEGSSSEAIANRIALIKSOLETTTSDPR 360
Db 301 SDLELEKATMTALGQAKITVDKSTVIYEGSSSEAIANRIALIKSOLETTTSDPR 360
Qy 361 EKLOERLAKLAGVAVIKVGAETELKEMKLRIEDALNATRAVEEGIVAGGCTALTIV 420
Db 361 EKLOERLAKLAGVAVIKVGAETELKEMKLRIEDALNATRAVEEGIVAGGCTALTIV 420
Qy 421 IEKVVALEEGDDA-TGRNIVYRALPEEPYQIALNAGYSGSVYIDKLKNSPAGTFNATG 476
Db 421 MKSIQIVGDEDEAETGVYIKVKAAGAPVQIALNAGYSGSVYIDKLKNSPAGTFNATG 476
Qy 479 TGEVDMKTIIDPVKYVTSALONASVASLITTEVAANKPEPATPAMPACMDPGM 532
Db 481 TKNMNVNWDAGIVDPKYVTSALONASVASLITTEVAANKPEPATPAMPACMDPGM 540
Qy 533 AGM 535
Db 541 MGM 543

RESULT 14
Qy 099SL7 PRELIMINARY: PRT: 538 AA.
AC 099SL7: 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
GN GROEL OR SAV2029 OR SA1896.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcaceae; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN (1)
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; Pubmed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-U Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hasekawa H., Kohara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Fuyuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC EMBL: AF003364; BAB58191.1;
DR HSP: P06139; IGR:
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP1.
DR Pfam: PF00118; Cpn60_TCP1.

```


* Wed Apr 16 08:08:22 2003

us-09-001-737-8.rspt

Page 9

DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
DR ATP-binding; Chapterone; Complete proteome.
SQ SEQUENCE 538 AA; 57572 MW; A3D8595603DC9313 CRC64;

Query Match 71.5%; Score 1905; DB 16; Length 538;
Best Local Similarity 69.8%; Pred. No. 1,1e-82;
Matches 377; Conservative 78; Mismatches 83; Indels 2; Gaps 2;

OY 1 MAKEIKFSADARAAMVRCVMDLADTVKVTGPGKRVNVEKAFGSPITNDGVTIAKEIE 60
DB 1 MVKQKFSADARAAMVRCVMDLADTVKVTGPGKRVNVEKAFGSPITNDGVTIAKEIE 60
OY 61 LEDPENNAGKLVGEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPVGIRGIE 120
DB 61 LEDPENNAGKLVGEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPVGIRGIE 120
OY 61 LEDPENNAGKLVGEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPVGIRGIE 120
DB 61 LEDPENNAGKLVGEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPVGIRGIE 120
OY 121 TATATAVEALKAIAQVSGKEATAOVAASRSSEKVEYISEAMERVNDGVITTEESRG 180
DB 121 TATATAVEALKAIAQVSGKEATAOVAASRSSEKVEYISEAMERVNDGVITTEESRG 180
OY 121 KAVKAVAEALHENSQVKNKEIAGVATSADEEIRISSEMEKVGNDGVITTEESRG 180
DB 121 KAVKAVAEALHENSQVKNKEIAGVATSADEEIRISSEMEKVGNDGVITTEESRG 180
OY 181 METELEVEGMOFDRGYLSQYMTDNEKNVADLENPILITDKVSNIDILPLEEVLK 240
DB 181 METELEVEGMOFDRGYLSQYMTDNEKNVADLENPILITDKVSNIDILPLEEVLK 240
OY 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVKAPGFGDRRKAMLEDIAIITGCVIT 300
DB 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVKAPGFGDRRKAMLEDIAIITGCVIT 300
OY 301 EDGLLEKDATMTALGOAKITVDKSTVIEGSSSEAIANRIALIKSOLETTTSDPDR 360
DB 301 EDGLLEKDATMTALGOAKITVDKSTVIEGSSSEAIANRIALIKSOLETTTSDPDR 360
OY 301 DDLGLDKDASIDMLGTASKVEVTKDNTVYDGDGSDNSIDARVSQLSIEETSDPDR 360
DB 301 DDLGLDKDASIDMLGTASKVEVTKDNTVYDGDGSDNSIDARVSQLSIEETSDPDR 360
OY 361 EKLOERLAKLAGVAVIVKGAAPTETALKEMKRIEDALNSTRAAVEGIVAGGITALIV 420
DB 361 EKLOERLAKLAGVAVIVKGAAPTETALKEMKRIEDALNSTRAAVEGIVAGGITALIV 420
OY 421 IEKVAALELEGDDATGRNIVYLALEPVRQIALNAGVBSVIVIKLNSPAGTGATG 480
DB 421 IEKVAALELEGDDATGRNIVYLALEPVRQIALNAGVBSVIVIKLNSPAGTGATG 480
OY 421 YKVSSEIEAGDLETCGVNIVYKALTAIPVROALNAGVBSVIVIKLNSPAGTGATG 480
DB 421 YKVSSEIEAGDLETCGVNIVYKALTAIPVROALNAGVBSVIVIKLNSPAGTGATG 480
OY 481 EYDMKITGIIIDPVKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 540
DB 481 EYDMKITGIIIDPVKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 540
OY 481 EYDMKITGIIIDPVKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 540
DB 481 EYDMKITGIIIDPVKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 540

RESULT 15

OBYTM6 PRELIMINARY; PRT; 525 AA.
AC OBYTM6; 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE GroEL.
OS Staphylococcus aureus
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RN4220.
RA Dugourd D.F., Young A., Wright J.A.;
RT "Molecular chaperones/chaperonin-encoding stress genes groEL and groES
and their use as antimicrobial targets."
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF325452; AAL56002.1;
DR InterPro; IPR001844; Chaprinin_Cpn60.
DR InterPro; IPR002423; Cpn60_TCP-1.
DR Pfam; PF00118; Cpn60_TCP1; 1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.

SQ SEQUENCE 525 AA; 56209 MW; 6FDB2249E9B78408 CRC64;

Query Match 70.9%; Score 1887; DB 2; Length 525;
Best Local Similarity 70.6%; Pred. No. 7.7e-82;
Matches 369; Conservative 78; Mismatches 76; Indels 0; Gaps 0;

OY 1 MAKEIKFSADARAAMVRCVMDLADTVKVTGPGKRVNVEKAFGSPITNDGVTIAKEIE 60
DB 1 MVKQKFSADARAAMVRCVMDLADTVKVTGPGKRVNVEKAFGSPITNDGVTIAKEIE 60
OY 61 LEDPENNAGKLVGEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPVGIRGIE 120
DB 61 LEDPENNAGKLVGEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPVGIRGIE 120
OY 61 LEDPENNAGKLVGEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPVGIRGIE 120
DB 61 LEDPENNAGKLVGEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPVGIRGIE 120
OY 121 TATATAVEALKAIAQVSGKEATAOVAASRSSEKVEYISEAMERVNDGVITTEESRG 180
DB 121 TATATAVEALKAIAQVSGKEATAOVAASRSSEKVEYISEAMERVNDGVITTEESRG 180
OY 121 KAVKAVAEALHENSQVKNKEIAGVATSADEEIRISSEMEKVGNDGVITTEESRG 180
DB 121 KAVKAVAEALHENSQVKNKEIAGVATSADEEIRISSEMEKVGNDGVITTEESRG 180
OY 181 METELEVEGMOFDRGYLSQYMTDNEKNVADLENPILITDKVSNIDILPLEEVLK 240
DB 181 METELEVEGMOFDRGYLSQYMTDNEKNVADLENPILITDKVSNIDILPLEEVLK 240
OY 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVKAPGFGDRRKAMLEDIAIITGCVIT 300
DB 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVKAPGFGDRRKAMLEDIAIITGCVIT 300
OY 301 EDGLLEKDATMTALGOAKITVDKSTVIEGSSSEAIANRIALIKSOLETTTSDPDR 360
DB 301 EDGLLEKDATMTALGOAKITVDKSTVIEGSSSEAIANRIALIKSOLETTTSDPDR 360
OY 301 DDLGLDKDASIDMLGTASKVEVTKDNTVYDGDGSDNSIDARVSQLSIEETSDPDR 360
DB 301 DDLGLDKDASIDMLGTASKVEVTKDNTVYDGDGSDNSIDARVSQLSIEETSDPDR 360
OY 361 EKLOERLAKLAGVAVIVKGAAPTETALKEMKRIEDALNSTRAAVEGIVAGGITALIV 420
DB 361 EKLOERLAKLAGVAVIVKGAAPTETALKEMKRIEDALNSTRAAVEGIVAGGITALIV 420
OY 421 IEKVAALELEGDDATGRNIVYLALEPVRQIALNAGVBSVIVIKLNSPAGTGATG 480
DB 421 IEKVAALELEGDDATGRNIVYLALEPVRQIALNAGVBSVIVIKLNSPAGTGATG 480
OY 421 YKVSSEIEAGDLETCGVNIVYKALTAIPVROALNAGVBSVIVIKLNSPAGTGATG 480
DB 421 YKVSSEIEAGDLETCGVNIVYKALTAIPVROALNAGVBSVIVIKLNSPAGTGATG 480
OY 481 EYDMKITGIIIDPVKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 523
DB 481 EYDMKITGIIIDPVKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 523

Search completed: April 8, 2003, 14:26:06
Job time : 41 secs